

Sequence Listing

<110> Botstein,David
Desnoyers,Luc
Ferrara,Napoleone
Fong,Sherman
Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
Tumas,Daniel
Watanabe,Colin K.
Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

<130> P2930R1C5

<150> 60/095,325

<151> 1998-08-04

<150> 60/112,851

<151> 1998-12-16

<150> 60/113,145

<151> 1998-12-16

<150> 60/113,511

<151> 1998-12-22

<150> 60/115,558

<151> 1999-01-12

<150> 60/115,565

<151> 1999-01-12

<150> 60/115,733

<151> 1999-01-12

<150> 60/119,341

<151> 1999-02-09

<151> 2000-03-03

<150> PCT/US99/12252

<151> 1999-06-02

<150> PCT/US99/28634

<151> 1999-12-01

<150> PCT/US99/28551

<151> 1999-12-02

<150> PCT/US00/03565

<151> 2000-02-11

<150> PCT/US00/04414

<151> 2000-02-22

<150> PCT/US00/05841

<151> 2000 -03-02

<150> PCT/US00/08439

<151> 2000-03-30

<150> PCT/US00/14941

<151> 2000-05-30

<150> PCT/US00/15264

<151> 2000-06-02

<150> PCT/US00/32678

<151> 2000-12-01

<140> US 09/866,034

<141> 2001-05-25

<160> 38

<210> 1

<211> 1283

<212> DNA

<213> Homo sapiens

<400> 1

cggacgcgtg ggaccatac ttgctggtct gatccatgca caaggcgggg 50
ctgctaggcc tctgtgcccg ggcttggaat tcggtgcgga tggccagctc 100
cgggatgacc cgccgggacc cgctcgcaaa taagggtggcc ctggtaacgg 150
cctccaccga cgggatcggc ttgccatcg cccggcgttt ggcccaggac 200
ggggcccatg tggtcgtcag cagccggaag cagcagaatg tggaccaggc 250
ggtggccacg ctgcaggggg aggggctgag cgtgacgggc accgtgtgcc 300
atgtggggaa ggcgaggac cgggagcggc tgggtggccac ggctgtgaag 350

cttcatggag gtatcgatat cctagtctcc aatgctgctg tcaacccttt 400
 ctttggaagc ataatggatg tcaactgagga ggtgtggggac aagactctgg 450
 acattaatgt gaaggcccca gccctgatga caaaggcagt ggtgccagaa 500
 atggagaaac gaggaggcgg ctcaagtggg atcgtgtctt ccatagcagc 550
 cttcagtcca tctcctgggt tcagtcctta caatgtcagt aaaacagcct 600
 tgctgggcct gaccaagacc ctggccatag agctggcccc aaggaacatt 650
 aggggtgaact gcttagcacc tggacttata aagactagct tcagcaggat 700
 gctctggatg gacaagggaa aagaggaaag catgaaagaa accctgcgga 750
 taagaagggt aggcgagcca gaggattgtg ctggcatcgt gtctttcctg 800
 tgctctgaag atgccagcta catcactggg gaaacagtgg tgggtgggtgg 850
 aggaaccccg tcccgctctt gaggaccggg agacagccca caggccagag 900
 ttgggtctta gctcctgggt ctgttctctg attcaccac tggectttcc 950
 cacctctgct cacttactg ttacctcat caaatcagtt ctgcctctgt 1000
 aaaagatcca gccttcctg ccgtcaaggt ggcgtcttac tggggattcc 1050
 tgctgttgtt gtggccttgg gtaaaagcct cccctgagaa cacaggacag 1100
 gcctgctgac aaggctgagt ctaccttggc aaagaccaag atattttttc 1150
 ctgggccact ggtgaatctg aggggtgatg ggagagaagg aacctggagt 1200
 ggaaggagca gagttgcaaa ttaacagctt gcaaatgagg tgcaataaaa 1250
 atgcagatga ttgcgcggtt ttgaaaaaaa aaa 1283

<210> 2
 <211> 278
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met His Lys Ala Gly Leu Leu Gly Leu Cys Ala Arg Ala Trp Asn
 1 5 10 15
 Ser Val Arg Met Ala Ser Ser Gly Met Thr Arg Arg Asp Pro Leu
 20 25 30
 Ala Asn Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly
 35 40 45
 Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
 50 55 60
 Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
 65 70 75

Leu Gln Gly Glu Gly Leu Ser Val Thr Gly Thr Val Cys His Val
80 85 90

Gly Lys Ala Glu Asp Arg Glu Arg Leu Val Ala Thr Ala Val Lys
95 100 105

Leu His Gly Gly Ile Asp Ile Leu Val Ser Asn Ala Ala Val Asn
110 115 120

Pro Phe Phe Gly Ser Ile Met Asp Val Thr Glu Glu Val Trp Asp
125 130 135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
140 145 150

Ala Val Val Pro Glu Met Glu Lys Arg Gly Gly Gly Ser Val Val
155 160 165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
170 175 180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
185 190 195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
200 205 210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
215 220 225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
230 235 240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
245 250 255

Cys Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val
260 265 270

Gly Gly Gly Thr Pro Ser Arg Leu
275

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 3

gcataatgga tgtcactgag g 21

<210> 4

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 4
agaacaatcc tgctgaaagc tag 23

<210> 5
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 5
gaaacgagga ggcggtcag tggatgatcgt gtcttcata gcagcc 46

<210> 6
<211> 3121
<212> DNA
<213> Homo sapiens

<400> 6
gcgccttgag ctccgcctcc gggcccgata gcggcatcga gagcgccctc 50
gtcgaggacc aggcggcgca gggggccggc gggcgaaagg aggatgaggg 100
ggcgcagcag ctgctgaccc tgcagaacca ggtggcgcggt ctggaggagg 150
agaaccgaga cttttctggct gcgctggagg acgccatgga gcagtacaaa 200
ctgcagagcg accggctggt tgagcagcag gaggagatgg tggaaactggt 250
gttgccgttta gagctggtgc ggccaggctg ggggggacct cggctcctga 300
atggcctgcc tcccggttcc tttgtgcctc gacctcctac agccccctg 350
gggggtgccc acgcccatgt gctgggcctg gtgccgcctg cctgcctccc 400
tgagatgaa gttggtctct agcagagggg agagcaggtg acaaattggc 450
gggaggctgg agctgagttg ctgactgagg tgaacaggct gggaagtggc 500
tcttcagctg cttcagagga ggaagaggag gaggaggagc cggccaggcg 550
gaccttacac ctgcgcagaa ataggatcag caactgcagt cagagggcgg 600
gggcacgccc agggagtctg ccagagagga agggcccgaga gctttgctt 650
gaggagtggg atgcagccat tccagggtcc agagcagttg gtgggagcaa 700
ggcccagatt caggcccgcc aggtcccccc tggcacagcc tcagagtggc 750
ggctggccca ggccagcag aagatccggg agctggctat caacatccgc 800
atgaaggagg agcttattgg cgagctggtc cgcacaggaa aggcagctca 850
ggccctgaac cgccagcaca gccagcgtat ccgggagctg gagcaggagg 900

cagagcaggt gcgggccgag ctgagtgaag gccagaggca gctgcgggag 950
 ctcgagggca aggagctcca ggatgctggc gagcggcttc ggctccagga 1000
 gttccgcagg agggctcgctg cggcccagag ccagggtgcag gtgctgaagg 1050
 agaagaagca ggctacggag cggctggtgt cactgtcggc ccagagtgaag 1100
 aagcgactgc aggagctcga gcggaacgtg cagctcatgc ggcagcagca 1150
 gggacagctg cagaggcgcc ttccgcagga gacggagcag aagcggcgcc 1200
 tggaggcaga aatgagcaag cggcagcacc gcgtcaagga gctggagctg 1250
 aagcatgagc aacagcagaa gatcctgaag attaagacgg aagagatcgc 1300
 ggccttcag aggaagaggc gcagtggcag caacggctct gtggtcagcc 1350
 tggaaacagca gcagaagatt gaggagcaga agaagtggct ggaccaggag 1400
 atggagaagg tgctacagca gcggcgggcg ctggaggagc tgggggagga 1450
 gctccacaag cgggaggcca tcctggccaa gaaggaggcc ctgatgcagg 1500
 agaagacggg gctggagagc aagcgctga gatccagcca ggccctcaac 1550
 gaggacatcg tgcgagtgtc cagccggctg gaggacctgg agaaggagct 1600
 gtccgagaag agcgggcagc tgcgagcagg cagcgcccag agccagcagc 1650
 agatccgcgg ggagatcgac agcctgcgcc aggagaagga ctgcgtgctc 1700
 aagcagcgcc tggagatcga cggcaagctg aggcagggga gtctgctgtc 1750
 ccccgaggag gagcggacgc tgttccagtt ggatgaggcc atcgaggccc 1800
 tggatgctgc cattgagtat aagaatgagg ccacacatg ccgccagcgg 1850
 gtgcttcggg cctcagcctc gttgctgtcc cagtgcgaga tgaacctcat 1900
 ggccaagctc agctacctct catcctcaga gaccagagcc ctctctgca 1950
 agtatattga caagggtgtg acgctccgag aggagcagca ccagcagcag 2000
 attgccttct cggaaactgga gatgcagctg gaggagcagc agaggctggt 2050
 gtactggctg gaggtggccc tggagcggca gcgcctggag atggaccgcc 2100
 agctgaccct gcagcagaag gagcacgagc agaacatgca gctgctcctg 2150
 cagcagagtc gagaccacct cggatgaagg ttagcagaca gcaggaggca 2200
 gtatgaggcc cggattcaag ctctggagaa ggaactgggc cgttacatgt 2250
 ggataaacca ggaactgaaa cagaagctcg gcggtgtgaa cgctgtaggc 2300
 cacagcaggg gtggggagaa gaggagcctg tgctcggagg gcagacaggc 2350

1-2 3-4 5-6 7-8 9-10 11-12 13-14 15-16 17-18 19-20 21-22 23-24 25-26 27-28 29-30 31-32 33-34 35-36 37-38 39-40 41-42 43-44 45-46 47-48 49-50 51-52 53-54 55-56 57-58 59-60 61-62 63-64 65-66 67-68 69-70 71-72 73-74 75-76 77-78 79-80 81-82 83-84 85-86 87-88 89-90 91-92 93-94 95-96 97-98 99-100 101-102 103-104 105-106 107-108 109-110 111-112 113-114 115-116 117-118 119-120 121-122 123-124 125-126 127-128 129-130 131-132 133-134 135-136 137-138 139-140 141-142 143-144 145-146 147-148 149-150 151-152 153-154 155-156 157-158 159-160 161-162 163-164 165-166 167-168 169-170 171-172 173-174 175-176 177-178 179-180 181-182 183-184 185-186 187-188 189-190 191-192 193-194 195-196 197-198 199-200 201-202 203-204 205-206 207-208 209-210 211-212 213-214 215-216 217-218 219-220 221-222 223-224 225-226 227-228 229-230 231-232 233-234 235-236 237-238 239-240 241-242 243-244 245-246 247-248 249-250 251-252 253-254 255-256 257-258 259-260 261-262 263-264 265-266 267-268 269-270 271-272 273-274 275-276 277-278 279-280 281-282 283-284 285-286 287-288 289-290 291-292 293-294 295-296 297-298 299-300 301-302 303-304 305-306 307-308 309-310 311-312 313-314 315-316 317-318 319-320 321-322 323-324 325-326 327-328 329-330 331-332 333-334 335-336 337-338 339-340 341-342 343-344 345-346 347-348 349-350 351-352 353-354 355-356 357-358 359-360 361-362 363-364 365-366 367-368 369-370 371-372 373-374 375-376 377-378 379-380 381-382 383-384 385-386 387-388 389-390 391-392 393-394 395-396 397-398 399-400 401-402 403-404 405-406 407-408 409-410 411-412 413-414 415-416 417-418 419-420 421-422 423-424 425-426 427-428 429-430 431-432 433-434 435-436 437-438 439-440 441-442 443-444 445-446 447-448 449-450 451-452 453-454 455-456 457-458 459-460 461-462 463-464 465-466 467-468 469-470 471-472 473-474 475-476 477-478 479-480 481-482 483-484 485-486 487-488 489-490 491-492 493-494 495-496 497-498 499-500 501-502 503-504 505-506 507-508 509-510 511-512 513-514 515-516 517-518 519-520 521-522 523-524 525-526 527-528 529-530 531-532 533-534 535-536 537-538 539-540 541-542 543-544 545-546 547-548 549-550 551-552 553-554 555-556 557-558 559-560 561-562 563-564 565-566 567-568 569-570 571-572 573-574 575-576 577-578 579-580 581-582 583-584 585-586 587-588 589-590 591-592 593-594 595-596 597-598 599-600 601-602 603-604 605-606 607-608 609-610 611-612 613-614 615-616 617-618 619-620 621-622 623-624 625-626 627-628 629-630 631-632 633-634 635-636 637-638 639-640 641-642 643-644 645-646 647-648 649-650 651-652 653-654 655-656 657-658 659-660 661-662 663-664 665-666 667-668 669-670 671-672 673-674 675-676 677-678 679-680 681-682 683-684 685-686 687-688 689-690 691-692 693-694 695-696 697-698 699-700 701-702 703-704 705-706 707-708 709-710 711-712 713-714 715-716 717-718 719-720 721-722 723-724 725-726 727-728 729-730 731-732 733-734 735-736 737-738 739-740 741-742 743-744 745-746 747-748 749-750 751-752 753-754 755-756 757-758 759-760 761-762 763-764 765-766 767-768 769-770 771-772 773-774 775-776 777-778 779-780 781-782 783-784 785-786 787-788 789-790 791-792 793-794 795-796 797-798 799-800 801-802 803-804 805-806 807-808 809-810 811-812 813-814 815-816 817-818 819-820 821-822 823-824 825-826 827-828 829-830 831-832 833-834 835-836 837-838 839-840 841-842 843-844 845-846 847-848 849-850 851-852 853-854 855-856 857-858 859-860 861-862 863-864 865-866 867-868 869-870 871-872 873-874 875-876 877-878 879-880 881-882 883-884 885-886 887-888 889-890 891-892 893-894 895-896 897-898 899-900 901-902 903-904 905-906 907-908 909-910 911-912 913-914 915-916 917-918 919-920 921-922 923-924 925-926 927-928 929-930 931-932 933-934 935-936 937-938 939-940 941-942 943-944 945-946 947-948 949-950 951-952 953-954 955-956 957-958 959-960 961-962 963-964 965-966 967-968 969-970 971-972 973-974 975-976 977-978 979-980 981-982 983-984 985-986 987-988 989-990 991-992 993-994 995-996 997-998 999-1000

tcttggaat gaagatgagc tccacctggc acccgagctt ctctggctgt 2400
 ccccccctcac tgaggggggccc ccccgacccc gggaggagac gcgggacttg 2450
 gtccacgctc cgttaccctt gacctggaaa cgctcgagcc tgtgtggtga 2500
 ggagcagggg tcccccgagg aactgaggca gcgggaggcg gctgagcccc 2550
 tggtagggcg ggtgcttctt gtgggtgagg caggcctgcc ctggaacttt 2600
 gggcctttgt ccaagccccg gcgggaactg cgacgagcca gcccggggat 2650
 gattgatgtc cggaaaaaacc ccctgtaagc cctcggggca gacctgctt 2700
 tggagggaga ctccgagcct gctgaaaggg gcagctgcct gttttgcttc 2750
 tgtgaagggc agtccctacc gcacacccta aatccaggcc ctcatctgta 2800
 cctcactgg gatcaacaaa tttgggccat ggcccaaaag aactggaccc 2850
 tcatttaaca aaataatatg caaattccca ccacttactt ccatgaagct 2900
 gtggtaccca attgccgctt tgtgtcttgc tcgaatctca ggacaattct 2950
 ggtttcaggc gtaaatggat gtgctttag ttcaggggtt tggccaagaa 3000
 tcatcacgaa agggctgggtg gcaaccagggt tgtggtttaa atggtcttat 3050
 gtatataggg gaaactggga gactttagga tcttaaaaaa ccatttaata 3100
 aaaaaaatc tttgaaggga c 3121

<210> 7
 <211> 830
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Glu Gln Tyr Lys Leu Gln Ser Asp Arg Leu Arg Glu Gln Gln
 1 5 10 15
 Glu Glu Met Val Glu Leu Arg Leu Arg Leu Glu Leu Val Arg Pro
 20 25 30
 Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser
 35 40 45
 Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala
 50 55 60
 His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu
 65 70 75
 Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu
 80 85 90
 Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly
 95 100 105

Ser Ser Ala Ala	Ser Glu Glu Glu Glu Glu Glu Glu Glu	Pro Pro
110	115	120
Arg Arg Thr Leu	His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser	
125	130	135
Gln Arg Ala Gly	Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly	
140	145	150
Pro Glu Leu Cys	Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser	
155	160	165
Arg Ala Val Gly	Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val	
170	175	180
Pro Pro Ala Thr	Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln	
185	190	195
Lys Ile Arg Glu	Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu	
200	205	210
Ile Gly Glu Leu	Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn	
215	220	225
Arg Gln His Ser	Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu	
230	235	240
Gln Val Arg Ala	Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu	
245	250	255
Leu Glu Gly Lys	Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu	
260	265	270
Gln Glu Phe Arg	Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln	
275	280	285
Val Leu Lys Glu	Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu	
290	295	300
Ser Ala Gln Ser	Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val	
305	310	315
Gln Leu Met Arg	Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg	
320	325	330
Glu Glu Thr Glu	Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys	
335	340	345
Arg Gln His Arg	Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln	
350	355	360
Gln Lys Ile Leu	Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln	
365	370	375
Arg Lys Arg Arg	Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu	
380	385	390
Gln Gln Gln Lys	Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu	

395	400	405
Met Glu Lys Val Leu Gln Gln Arg Arg	Ala Leu Glu Glu Leu Gly	
410	415	420
Glu Glu Leu His Lys Arg Glu Ala Ile	Leu Ala Lys Lys Glu Ala	
425	430	435
Leu Met Gln Glu Lys Thr Gly Leu Glu	Ser Lys Arg Leu Arg Ser	
440	445	450
Ser Gln Ala Leu Asn Glu Asp Ile Val	Arg Val Ser Ser Arg Leu	
455	460	465
Glu His Leu Glu Lys Glu Leu Ser Glu	Lys Ser Gly Gln Leu Arg	
470	475	480
Gln Gly Ser Ala Gln Ser Gln Gln Gln	Ile Arg Gly Glu Ile Asp	
485	490	495
Ser Leu Arg Gln Glu Lys Asp Ser Leu	Leu Lys Gln Arg Leu Glu	
500	505	510
Ile Asp Gly Lys Leu Arg Gln Gly Ser	Leu Leu Ser Pro Glu Glu	
515	520	525
Glu Arg Thr Leu Phe Gln Leu Asp Glu	Ala Ile Glu Ala Leu Asp	
530	535	540
Ala Ala Ile Glu Tyr Lys Asn Glu Ala	Ile Thr Cys Arg Gln Arg	
545	550	555
Val Leu Arg Ala Ser Ala Ser Leu Leu	Ser Gln Cys Glu Met Asn	
560	565	570
Leu Met Ala Lys Leu Ser Tyr Leu Ser	Ser Ser Glu Thr Arg Ala	
575	580	585
Leu Leu Cys Lys Tyr Phe Asp Lys Val	Val Thr Leu Arg Glu Glu	
590	595	600
Gln His Gln Gln Gln Ile Ala Phe Ser	Glu Leu Glu Met Gln Leu	
605	610	615
Glu Glu Gln Gln Arg Leu Val Tyr Trp	Leu Glu Val Ala Leu Glu	
620	625	630
Arg Gln Arg Leu Glu Met Asp Arg Gln	Leu Thr Leu Gln Gln Lys	
635	640	645
Glu His Glu Gln Asn Met Gln Leu Leu	Leu Gln Gln Ser Arg Asp	
650	655	660
His Leu Gly Glu Gly Leu Ala Asp Ser	Arg Arg Gln Tyr Glu Ala	
665	670	675
Arg Ile Gln Ala Leu Glu Lys Glu Leu	Gly Arg Tyr Met Trp Ile	
680	685	690

Asn	Gln	Glu	Leu	Lys	Gln	Lys	Leu	Gly	Gly	Val	Asn	Ala	Val	Gly	695	700	705
His	Ser	Arg	Gly	Gly	Glu	Lys	Arg	Ser	Leu	Cys	Ser	Glu	Gly	Arg	710	715	720
Gln	Ala	Pro	Gly	Asn	Glu	Asp	Glu	Leu	His	Leu	Ala	Pro	Glu	Leu	725	730	735
Leu	Trp	Leu	Ser	Pro	Leu	Thr	Glu	Gly	Ala	Pro	Arg	Thr	Arg	Glu	740	745	750
Glu	Thr	Arg	Asp	Leu	Val	His	Ala	Pro	Leu	Pro	Leu	Thr	Trp	Lys	755	760	765
Arg	Ser	Ser	Leu	Cys	Gly	Glu	Glu	Gln	Gly	Ser	Pro	Glu	Glu	Leu	770	775	780
Arg	Gln	Arg	Glu	Ala	Ala	Glu	Pro	Leu	Val	Gly	Arg	Val	Leu	Pro	785	790	795
Val	Gly	Glu	Ala	Gly	Leu	Pro	Trp	Asn	Phe	Gly	Pro	Leu	Ser	Lys	800	805	810
Pro	Arg	Arg	Glu	Leu	Arg	Arg	Ala	Ser	Pro	Gly	Met	Ile	Asp	Val	815	820	825
Arg	Lys	Asn	Pro	Leu											830		

<210> 8
 <211> 662
 <212> DNA
 <213> Homo sapiens

<400> 8
 attctcctag agcatctttg gaagcatgag gccacgatgc tgcattcttg 50
 ctcttggtctg ctggataaca gtcttctctcc tccagtgttc aaaaggaact 100
 acagacgctc ctgttggtgc aggactgtgg ctgtgccagc cgacacccag 150
 gtgtgggaac aagatctaca acccttcaga gcagtgtgt tatgatgatg 200
 ccatcttate cttaaaggag acccgccgct gtggctccac ctgcaccttc 250
 tggccctgct ttgagctctg ctgtcccgag tcttttgcc cccagcagaa 300
 gtttcttggtg aagttgaggg ttctgggtat gaagtctcag tgtcacttat 350
 ctcccatctc ccggagctgt accaggaaca ggaggcacgt cctgtaccca 400
 taaaaacccc aggctccact ggcagacggc agacaagggg agaagagacg 450
 aagcagctgg acatcggaga ctacagttga acttcggaga gaagcaactt 500
 gacttcagag ggatggctca atgacatagc ttgggagagg agcccagctg 550

gggatggcca gacttcaggg gaagaatgcc ttctgcttc atcccccttc 600
 cagctccctt tcccgctgag agccactttc atcggaata aaatccccca 650
 cattaccat ct 662

<210> 9
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr
 1 5 10 15
 Val Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val
 20 25 30
 Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
 35 40 45
 Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
 50 55 60
 Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
 65 70 75
 Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
 80 85 90
 Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
 95 100 105
 Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
 110 115 120
 His Val Leu Tyr Pro
 125

<210> 10
 <211> 1942
 <212> DNA
 <213> Homo sapiens

<400> 10
 cccacgcgtc cgcccacgag tccgggtgcc actcgcgcgc cgcccgcgct 50
 ccgggcttct cttttccctc cgacgcgcca cggctgcccc gacattccgg 100
 ctgcggggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150
 ggcgccaggg tggcccccg ggcgcgcttg gtctcgga gaagcgggacg 200
 agggcgagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250
 ggccgcgact accggcagct gacagcgaga tgagcgactc ccagagacg 300
 ccctagcccc gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350

ttagtggtcc gccccacgcg ggtcgccggc cggcccagga tgggcgctgg 400
 caaccggggc ccgcgcccgc cgtgctacc cctgcgcccg ctgcgagccc 450
 ggcgtccggc ccgcgccttg cgtcatgga cggcggtcc cggctggcgg 500
 cggcgcgccc cggggtgtg aatgcgaact gcccctcggc cgcgctcccc 550
 gcccgcgcgc ccgcggggac gtggtagggg atgcccagct cactgogat 600
 ggcagttggc gcgctctcca gttccctcct ggtcacctgc tgctgatgg 650
 tggtctgtg cagtccgagc atcccgtgg agaagctggc ccaggcacca 700
 gagcagccgg gccaggagaa gcgtgagcac gccactcggg acggcccggg 750
 gcgggtgaac gagctcgggc gcccgggag ggacgagggc ggcagcggcc 800
 gggactggaa gagcaagagc ggcgtgggc tcgcccggcg tgagccgtgg 850
 agcaagctga agcaggcctg ggtctcccag ggcgggggcg ccaaggccgg 900
 ggatctgcag gtccggcccc gcggggacac ccgcgaggcg gaagccctgg 950
 ccgcagccgc ccaggacgcg attggcccgg aactcgcgc cagcccagag 1000
 ccaccgagg agtacgtgta cccggactac cgtggcaagg gctgcgtgga 1050
 cgagagcggc ttcgtgtacg cgatcgggga gaagttcgcg ccgggccccct 1100
 cggcctgccc gtgcctgtgc accgaggagg ggccgctgtg cgcgcagccc 1150
 gagtgcgcga ggctgcacc gcgctgcac cactgcaca cgagccagtg 1200
 ctgcccgcag tgcaaggaga ggaagaacta ctgcgagttc cggggcaaga 1250
 cctatcagac tttggaggag ttcgtggtgt ctccatgcga gaggtgtcgc 1300
 tgtgaagcca acggtgaggt gctatgcaca gtgtcagcgt gtccccagac 1350
 ggagtgtgtg gaccctgtgt acgagcctga tcagtgtgt cccatctgca 1400
 aaaatggtcc aaactgcttt gcagaaaccg cggatgatccc tgctggcaga 1450
 gaagtgaaga ctgacgagtg caccatatgc cactgtactt atgaggaagg 1500
 cacatggaga atcgagcggc aggccatgtg cagagacat gaatgcaggc 1550
 aaatgtagac gttcccaga acacaaactc tgactttttc tagaacattt 1600
 tactgatgtg aacattctag atgactctgg gaactatcag tcaaagaaga 1650
 cttttgatga ggaataatgg aaaattgttg gtacttttcc ttttcttgat 1700
 aacagttact acaacagaag gaaatggata tatttcaaaa catcaacaag 1750
 aactttgggc ataaaaatcct tctctaaata aatgtgctat tttcacagta 1800

agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850
cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900
gtgttgtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 11

<211> 325

<212> PRT

<213> Homo sapiens

<400> 11

Met	Pro	Ser	Ser	Thr	Ala	Met	Ala	Val	Gly	Ala	Leu	Ser	Ser	Ser	1	5	10	15
Leu	Leu	Val	Thr	Cys	Cys	Leu	Met	Val	Ala	Leu	Cys	Ser	Pro	Ser	20	25	30	
Ile	Pro	Leu	Glu	Lys	Leu	Ala	Gln	Ala	Pro	Glu	Gln	Pro	Gly	Gln	35	40	45	
Glu	Lys	Arg	Glu	His	Ala	Thr	Arg	Asp	Gly	Pro	Gly	Arg	Val	Asn	50	55	60	
Glu	Leu	Gly	Arg	Pro	Ala	Arg	Asp	Glu	Gly	Gly	Ser	Gly	Arg	Asp	65	70	75	
Trp	Lys	Ser	Lys	Ser	Gly	Arg	Gly	Leu	Ala	Gly	Arg	Glu	Pro	Trp	80	85	90	
Ser	Lys	Leu	Lys	Gln	Ala	Trp	Val	Ser	Gln	Gly	Gly	Gly	Ala	Lys	95	100	105	
Ala	Gly	Asp	Leu	Gln	Val	Arg	Pro	Arg	Gly	Asp	Thr	Pro	Gln	Ala	110	115	120	
Glu	Ala	Leu	Ala	Ala	Ala	Ala	Gln	Asp	Ala	Ile	Gly	Pro	Glu	Leu	125	130	135	
Ala	Pro	Thr	Pro	Glu	Pro	Pro	Glu	Glu	Tyr	Val	Tyr	Pro	Asp	Tyr	140	145	150	
Arg	Gly	Lys	Gly	Cys	Val	Asp	Glu	Ser	Gly	Phe	Val	Tyr	Ala	Ile	155	160	165	
Gly	Glu	Lys	Phe	Ala	Pro	Gly	Pro	Ser	Ala	Cys	Pro	Cys	Leu	Cys	170	175	180	
Thr	Glu	Glu	Gly	Pro	Leu	Cys	Ala	Gln	Pro	Glu	Cys	Pro	Arg	Leu	185	190	195	
His	Pro	Arg	Cys	Ile	His	Val	Asp	Thr	Ser	Gln	Cys	Cys	Pro	Gln	200	205	210	
Cys	Lys	Glu	Arg	Lys	Asn	Tyr	Cys	Glu	Phe	Arg	Gly	Lys	Thr	Tyr	215	220	225	
Gln	Thr	Leu	Glu	Glu	Phe	Val	Val	Ser	Pro	Cys	Glu	Arg	Cys	Arg				

230	235	240
Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro		
245	250	255
Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys		
260	265	270
Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val		
275	280	285
Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys		
290	295	300
His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala		
305	310	315
Met Cys Thr Arg His Glu Cys Arg Gln Met		
320	325	

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 12
 gaggtgtcgc tgtgaagcca acgg 24

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 13
 cgctcgattc tccatgtgcc ttcc 24

<210> 14
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 14
 gacggagtgt gtggaccctg tgtacgagcc tgatcagtgc tgtcc 45

<210> 15
 <211> 1587
 <212> DNA
 <213> Homo sapiens

<400> 15

cagccacaga cgggtcatga gcgcggtatt actgctggcc ctcttggggt 50
tcatectccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100
gttcagcatg tgtggaaggt gtccgaccta ccccggaat ggaccctaa 150
gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200
ttgagagcgg accccaagtg agcctgggtgc tctccaaggg ctgcacggag 250
gccaaggacc aggagccccg cgteactgag caccggatgg gccccggcct 300
ctcectgate tectacacct tegtgtgccg ccaggaggac ttctgcaaca 350
acctcgtaa ctccctcccg ctttggggccc cacagcccc agcagacca 400
ggatccttga ggtgccagt ctgcttgtct atggaaggct gtctggaggg 450
gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500
tctcaggct caggggagga ggcattctct ccaatctgag agtccaggga 550
tgcatgcccc agccagggtg caacctgctc aatgggacac aggaaattgg 600
gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650
atcgggggac caccattatg acacacggaa acttggctca agaaccact 700
gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750
ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800
caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850
cactcagccc ctcttggggt gcttgtggcc tctataccc acttctgctc 900
ctcggacctg tgcaatagt ccagcagcag cagcgttctg ctgaactccc 950
tccctcctca agctgcccc gtcccaggag accggcagtg tctacctgt 1000
gtgcagcccc ttggaacctg ttcaagtggc tcccccgaa tgacctgcc 1050
caggggcgcc actcattgtt atgatgggtta cattcatctc tcaggagggtg 1100
ggctgtccac caaaatgagc attcagggt gcgtggccca acctccagc 1150
ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200
gcgtgatgtg cagcctctg cctctcagca tgaggaggt ggggctgagg 1250
gcctggagtc tctcacttg ggggtggggc tggcactggc cccagcgtg 1300
tggtggggag tggtttggcc ttctgctaa ctctattacc cccacgatc 1350
ttcacgctg ctgaccaccc aactcaacc tccctctgac ctcataacct 1400
aatggccttg gacaccagat tcttcccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500
gacctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550
gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 16
<211> 437
<212> PRT
<213> Homo sapiens

<400> 16

Met	Ser	Ala	Val	Leu	Leu	Leu	Ala	Leu	Leu	Gly	Phe	Ile	Leu	Pro	1	5	10	15
Leu	Pro	Gly	Val	Gln	Ala	Leu	Leu	Cys	Gln	Phe	Gly	Thr	Val	Gln	20	25	30	
His	Val	Trp	Lys	Val	Ser	Asp	Leu	Pro	Arg	Gln	Trp	Thr	Pro	Lys	35	40	45	
Asn	Thr	Ser	Cys	Asp	Ser	Gly	Leu	Gly	Cys	Gln	Asp	Thr	Leu	Met	50	55	60	
Leu	Ile	Glu	Ser	Gly	Pro	Gln	Val	Ser	Leu	Val	Leu	Ser	Lys	Gly	65	70	75	
Cys	Thr	Glu	Ala	Lys	Asp	Gln	Glu	Pro	Arg	Val	Thr	Glu	His	Arg	80	85	90	
Met	Gly	Pro	Gly	Leu	Ser	Leu	Ile	Ser	Tyr	Thr	Phe	Val	Cys	Arg	95	100	105	
Gln	Glu	Asp	Phe	Cys	Asn	Asn	Leu	Val	Asn	Ser	Leu	Pro	Leu	Trp	110	115	120	
Ala	Pro	Gln	Pro	Pro	Ala	Asp	Pro	Gly	Ser	Leu	Arg	Cys	Pro	Val	125	130	135	
Cys	Leu	Ser	Met	Glu	Gly	Cys	Leu	Glu	Gly	Thr	Thr	Glu	Glu	Ile	140	145	150	
Cys	Pro	Lys	Gly	Thr	Thr	His	Cys	Tyr	Asp	Gly	Leu	Leu	Arg	Leu	155	160	165	
Arg	Gly	Gly	Gly	Ile	Phe	Ser	Asn	Leu	Arg	Val	Gln	Gly	Cys	Met	170	175	180	
Pro	Gln	Pro	Gly	Cys	Asn	Leu	Leu	Asn	Gly	Thr	Gln	Glu	Ile	Gly	185	190	195	
Pro	Val	Gly	Met	Thr	Glu	Asn	Cys	Asn	Arg	Lys	Asp	Phe	Leu	Thr	200	205	210	
Cys	His	Arg	Gly	Thr	Thr	Ile	Met	Thr	His	Gly	Asn	Leu	Ala	Gln	215	220	225	
Glu	Pro	Thr	Asp	Trp	Thr	Thr	Ser	Asn	Thr	Glu	Met	Cys	Glu	Val				

230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu	Leu Ile Asp Val Gly Leu	
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly	Cys Ser Thr Val Gly Ala	
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His	Ser Ala Pro Pro Gly Val	
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn	
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu	Asn Ser Leu Pro Pro Gln	
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln	Cys Pro Thr Cys Val Gln	
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro	
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln	
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe	
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His	
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp	Trp Gly Val Val Cys Pro	
425	430	435

Ser Cys

<210> 17
 <211> 2387
 <212> DNA
 <213> Homo sapiens

<400> 17
 cgacgatgct acgcgcgccc ggetgcctcc tccggacctc cgtagcgcoot 50
 gccgcggccc tggctgcggc gctgctctcg tcgcttgccg gctgctctct 100
 tctagagccg agggaccccg tggcctcgtc gctcagcccc tatttccggca 150
 ccaagactcg ctacgaggat gtcaaccccg tgctattgtc gggccccgag 200

gctccgtggc gggaccctga gctgctggag gggaccctgca ccccggtgca 250
 gctgggtcgcc ctcatctgcc acggcaccgc ctacccacgc gtcaaacaga 300
 tccgcaagct gaggcagctg caagggttgc tgcaggccgc cgggtccagg 350
 gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagcgtggc 400
 cgactggcct ttgtgttacg cggactggat ggacgggcag ctagtagaga 450
 agggacggca ggatatgca cagctggcgc tgcgtctggc ctgctcttc 500
 cggccctttt tcagccgtga gaactacggc cgcctgcggc tcatcaccag 550
 ttccaagcac cgctgcatgg atagcagcgc cgccttcctg caggggctgt 600
 ggcagcacta ccaccctggc ttgcgcgcgc cggacgtcgc agatatggag 650
 tttggacctc caacagttaa tgataaacta atgagatttt ttgatcactg 700
 tgagaagttt ttaactgaag tagaaaaaaa tgctacagct ctttatcagc 750
 tggaagcctt caaaactgga ccagaaatgc agaacatttt aaaaaaagtt 800
 gcagctactt tgcaagtgc agtaaagat ttaaagtcag atttaattca 850
 agtagccttt ttcacctggt catttgacct ggcaattaaa ggtgttaaat 900
 ctcttggtg tgatgttttt gacatagatg atgcaaaggt attagaatat 950
 ttaaagatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000
 cagtcgatcc agctgcacct tgtttcagga tatctttcag cacttggaca 1050
 aagcagttga acagaaacaa aggtctcagc caatttcttc tccagtcac 1100
 ctccagtttg gtcatgcaga gactcttctt cactgcttt ctctcatggg 1150
 ctacttcaaa gacaaggac ccctaacagc gtacaattac aaaaaacaaa 1200
 tgcacggaa gttccgaagt ggtctcattg taccttatgc ctggaacctg 1250
 atatttgtgc ttaccactg tgaaaatgct aagactccta aagaacaatt 1300
 ccgagtgcag atgttattaa atgaaaaggt gttacctttg gcttactcac 1350
 aagaaactgt ttcattttat gaagatctga agaaccacta caaggacac 1400
 cttcagagtt gtcaaaccag tgaagaatgt gaattagcaa gggctaacag 1450
 tacatctgat gaactatgag taactgaaga acatttttaa ttcttttagg 1500
 atctgcaatg agtgattaca tgcttgtaat aggtaggcaa ttccttgatt 1550
 acaggaagct tttatattac ttgagtattt ctgtcttttc acagaaaaac 1600
 attgggtttc tctctgggtt tggacatgaa atgtaagaaa agatttttca 1650

ctggagcagc tctcttaagg agaaacaaat ctatttagag aaacagctgg 1700
 ccctgcaaat gtttacagaa atgaaattct tctacttat ataagaaatc 1750
 tcacactgag atagaattgt gatttcataa taacacttga aaagtgtgg 1800
 agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850
 ggaactttac agattgttct gcagttctct cttcttttcc tcaggtagga 1900
 cagctctagc attttcttaa tcaggaatat tgtggtaagc tgggagtatc 1950
 actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000
 agtgttgtaa aaggacacct tcaactgaagc aagtcggaaa gtacaatgaa 2050
 aataaatatt tttggtattt atttatgaaa tatttgaaca ttttttcaat 2100
 aattcctttt tacttctagg aagtctcaaa agaccatctt aaattattat 2150
 atgtttggac aattagcaac aagtcagata gttagaatcg aagtttttca 2200
 aatccattgc ttagctaact ttttcattct gtcacttggc ttcgattttt 2250
 atattttcct attatatgaa atgtatcttt tgggtgtttg atttttcttt 2300
 ctttctttgt aaatagttct gagttctgtc aaatgccgtg aaagtatttg 2350
 ctataataaa gaaaattctt gtgacttttaa aaaaaaa 2387

<210> 18
 <211> 487
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Leu	Arg	Ala	Pro	Gly	Cys	Leu	Leu	Arg	Thr	Ser	Val	Ala	Pro
1				5					10					15
Ala	Ala	Ala	Leu	Ala	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Ala	Arg	Cys
			20						25					30
Ser	Leu	Leu	Glu	Pro	Arg	Asp	Pro	Val	Ala	Ser	Ser	Leu	Ser	Pro
			35						40					45
Tyr	Phe	Gly	Thr	Lys	Thr	Arg	Tyr	Glu	Asp	Val	Asn	Pro	Val	Leu
			50						55					60
Leu	Ser	Gly	Pro	Glu	Ala	Pro	Trp	Arg	Asp	Pro	Glu	Leu	Leu	Glu
			65						70					75
Gly	Thr	Cys	Thr	Pro	Val	Gln	Leu	Val	Ala	Leu	Ile	Arg	His	Gly
			80						85					90
Thr	Arg	Tyr	Pro	Thr	Val	Lys	Gln	Ile	Arg	Lys	Leu	Arg	Gln	Leu
			95						100					105
His	Gly	Leu	Leu	Gln	Ala	Arg	Gly	Ser	Arg	Asp	Gly	Gly	Ala	Ser

110	115	120
Ser Thr Gly Ser Arg Asp Leu Gly Ala	Ala Leu Ala Asp Trp Pro	
125	130	135
Leu Trp Tyr Ala Asp Trp Met Asp Gly	Gln Leu Val Glu Lys Gly	
140	145	150
Arg Gln Asp Met Arg Gln Leu Ala Leu	Arg Leu Ala Ser Leu Phe	
155	160	165
Pro Ala Leu Phe Ser Arg Glu Asn Tyr	Gly Arg Leu Arg Leu Ile	
170	175	180
Thr Ser Ser Lys His Arg Cys Met Asp	Ser Ser Ala Ala Phe Leu	
185	190	195
Gln Gly Leu Trp Gln His Tyr His Pro	Gly Leu Pro Pro Pro Asp	
200	205	210
Val Ala Asp Met Glu Phe Gly Pro Pro	Thr Val Asn Asp Lys Leu	
215	220	225
Met Arg Phe Phe Asp His Cys Glu Lys	Phe Leu Thr Glu Val Glu	
230	235	240
Lys Asn Ala Thr Ala Leu Tyr His Val	Glu Ala Phe Lys Thr Gly	
245	250	255
Pro Glu Met Gln Asn Ile Leu Lys Lys	Val Ala Ala Thr Leu Gln	
260	265	270
Val Pro Val Asn Asp Leu Asn Ala Asp	Leu Ile Gln Val Ala Phe	
275	280	285
Phe Thr Cys Ser Phe Asp Leu Ala Ile	Lys Gly Val Lys Ser Pro	
290	295	300
Trp Cys Asp Val Phe Asp Ile Asp Asp	Ala Lys Val Leu Glu Tyr	
305	310	315
Leu Asn Asp Leu Lys Gln Tyr Trp Lys	Arg Gly Tyr Gly Tyr Thr	
320	325	330
Ile Asn Ser Arg Ser Ser Cys Thr Leu	Phe Gln Asp Ile Phe Gln	
335	340	345
His Leu Asp Lys Ala Val Glu Gln Lys	Gln Arg Ser Gln Pro Ile	
350	355	360
Ser Ser Pro Val Ile Leu Gln Phe Gly	His Ala Glu Thr Leu Leu	
365	370	375
Pro Leu Leu Ser Leu Met Gly Tyr Phe	Lys Asp Lys Glu Pro Leu	
380	385	390
Thr Ala Tyr Asn Tyr Lys Lys Gln Met	His Arg Lys Phe Arg Ser	
395	400	405

110 115 120
 125 130 135
 140 145 150
 155 160 165
 170 175 180
 185 190 195
 200 205 210
 215 220 225
 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315
 320 325 330
 335 340 345
 350 355 360
 365 370 375
 380 385 390
 395 400 405

Gly	Leu	Ile	Val	Pro	Tyr	Ala	Ser	Asn	Leu	Ile	Phe	Val	Leu	Tyr
				410					415					420
His	Cys	Glu	Asn	Ala	Lys	Thr	Pro	Lys	Glu	Gln	Phe	Arg	Val	Gln
				425					430					435
Met	Leu	Leu	Asn	Glu	Lys	Val	Leu	Pro	Leu	Ala	Tyr	Ser	Gln	Glu
				440					445					450
Thr	Val	Ser	Phe	Tyr	Glu	Asp	Leu	Lys	Asn	His	Tyr	Lys	Asp	Ile
				455					460					465
Leu	Gln	Ser	Cys	Gln	Thr	Ser	Glu	Glu	Cys	Glu	Leu	Ala	Arg	Ala
				470					475					480
Asn	Ser	Thr	Ser	Asp	Glu	Leu								
				485										

<210> 19

<211> 3554

<212> DNA

<213> Homo sapiens

<400> 19

```

gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50
atggcgctga ggcgccacc gegactcggg ctctgcgctc ggctgcctga 100
cttcttctctg ctgtgctttt tcaggggctg cctgataggg gctgtaaatc 150
tcaaattccag caatcgaacc ccagtgggtac aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttgcagaca agtgaccca ggatcgagtg 250
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600
ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
acaggcactt tgggtgttcac tgetgttcac aaggacgact ctgggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750
agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800
gttgctcctg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850

```


tggcccttgc ttcattccagc acagctctca ggtgggcact gcagggacac 2350
 tgggtgtcttc catgtagcgt cccagctttg ggctcctgta acagacctct 2400
 ttttggttat ggatggctca caaaataggg cccccaatgc tttttttttt 2450
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500
 tgcgaaatca agtctgtcaa gtacaataac attttttaaaa gaaaatggat 2550
 cccactgttc ctctttgcc aagagaaagc acccagacgc cacaggctct 2600
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650
 aaagaacgtc aggtggagca gccagggtgaa aggcctggcg gggaggaaaag 2700
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750
 atccgccgga gacactgtc ccatttgtag ggggacatta gcaacatcac 2800
 tcagaagcct gtgtttctca agagcagggt ttctcagcct cacatgccct 2850
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcaccttgt 2950
 ctttcagctt ccagtgtctt ggggtttttta tactttgaca gctttttttt 3000
 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050
 tgccgcaggg cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100
 gctccctggt gtctgtgtca tggcactctg gatgcttagc atgcaagtgc 3150
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200
 ttggggatcc acgctccagc ctcttctctg gttgtcatag tgatagggta 3250
 gccttattgc cccctcttct tataccctaa aaccttctac actagtgcc 3300
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400
 aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450
 gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500
 caccgtaatt tggcatttgt ttaacctcat ttataaaaag ttcaaaaaaa 3550
 ccca 3554

<210> 20
 <211> 310
 <212> PRT
 <213> Homo sapiens
 <400> 20

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu	1	5	10	15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	20	25	30	
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	
His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His	200	205	210	
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala	215	220	225	
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu	230	235	240	
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val	245	250	255	
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly	260	265	270	
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro	275	280	285	
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly				

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300

290

295

300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
 305 310

<210> 21

<211> 3437

<212> DNA

<213> Homo sapiens

<400> 21

caggaccagg tcttctacg ctggagcagc ggggagacag ccaccatgca 50
 catectcgtg gtccatgccg tggatgacct gctgacgctg ggcccgccgc 100
 gagccgacga cagcgagttc caggcgctgc tggacatctg gtttccggag 150
 gagaagccac tgcccaccgc ctctctgggtg gacacatcgg aggagcgct 200
 gctgcttctt gactggctga agctgcgcct gatccgttct gaggtgctcc 250
 gcctgggtga cgcgcgccctg caggacctgg agccgcagca gctgctgctg 300
 ttctgtcagt cgtttggcat ccccggtgcc agcatgagca aactcctcca 350
 gtctctggac caggcagtgg cccacgacct ccagactctg gagcagaaca 400
 tcatggacaa gaattacatg gcccacctgg tggaggtcca gcatgagcgc 450
 ggcgccctcc gaggccagac ttccactccc ttgctcacag cctccctgcc 500
 gccccgccga gacagcacag aggcacccaa accaaagagc agcccagagc 550
 agcccatagg ccaggggccg attcgggtgg ggaccagct ccgggtgctg 600
 ggccctgagg acgacctggc tggcatgttc ctccagattt tcccgctcag 650
 cccggacctt cgggtggcaga gctccagtcc ccgccccctg gccctcgccc 700
 tgcagcaggc cctgggcccag gagctggccc gcgtcgtcca gggcagcccc 750
 gaggtgccgg gcatcacggt gcgtgtcttg caggccctcg ccaccctgct 800
 cagctcccca cagggcggtg ccttgggtgat gtccatgcac cgtagccact 850
 tcctggcctg cccgctgctg cgcagctctt gccagtacca gcgctgtgtg 900
 ccacaggaca ccggtctctc ctgctctctt ctgaaggtgc tcctgcagat 950
 gctgcagtgg ctggacagcc ctggcggtga gggcgggccc ctgcgggcac 1000
 agctcaggat gcttgccagc caggccctcag ccggggcgag gctcagtgat 1050
 gtgcgagggg ggctctcgcg cctggccgag gccctggcct tccgtcagga 1100
 cctggaggtg gtcagctcca ccgtccgtgc cgtcatcgcc accctgaggt 1150
 ctggggagca gtgcagcgtg gaggccgacc tgatcagcaa agtcctccag 1200

gggctgatcg	aggtgaggtc	ccccacctg	gaggagctgc	tgactgcatt	1250
cttctctgcc	actgcggatg	ctgctcccc	gtttccagcc	tgtaagcccc	1300
ttgtggtggt	gagctccctg	ctgctgcagg	aggaggagcc	cctggctggg	1350
gggaagccgg	gtgcggacgg	tggcagcctg	gaggccgtgc	ggctggggcc	1400
ctcgtcaggc	ctcctagtgg	actggctgga	aatgctggac	cccgaggtgg	1450
tcagcagctg	ccccgacctg	cagctcaggc	tgctcttctc	ccggaggaag	1500
ggcaaaggtc	aggcccaggt	gccctcgttc	cgccccacc	tcctgacctt	1550
cttcacgcat	cagtccagct	ggccccact	gcaccagtgc	atccgagtcc	1600
tgctgggcaa	gagccgggaa	cagaggttcg	acccctctgc	ctctctggac	1650
ttcctctggg	cctgcatcca	tgttcctcgc	atctggcagg	ggcgggacca	1700
gcgcaccccc	cagaagcggc	gggaggagct	ggtgctgcgg	gtccagggcc	1750
cggagctcat	cagcctggtg	gagctgatcc	tggccgaggc	ggagacgcgg	1800
agccaggacg	gggacacagc	cgctgcagc	ctcatccagg	ccgggctgcc	1850
cctgctgctc	agctgctgct	gtggggacga	tgagagtgtc	aggaaggtga	1900
cggagcacct	gtcaggctgc	atccagcagt	ggggagacag	cgtgctggga	1950
aggcgctgcc	gagaccttct	cctgcagctc	tacctacagc	ggccggagct	2000
gcgggtgccc	gtgcctgagg	tcctactgca	cagcgaaggg	gctgccagca	2050
gcagcgtctg	caagctggac	ggactcatcc	accgcttcac	cacgctcctt	2100
gcggacacca	gcgactcccc	ggcgttggag	aaccgagggg	cggatgccag	2150
catggcctgc	cggaagctgg	cggtggcgca	cccgtgctg	ctgctcaggc	2200
acctgcccac	gatcgcgggc	ctctgcacg	gccgcaccca	cctcaacttc	2250
caggagtctc	ggcagcagaa	ccacctgagc	tgcttcctgc	acgtgctggg	2300
cctgctggag	ctgctgcagc	cgcacgtggt	ccgcagcgag	caccaggggg	2350
cgctgtggga	ctgccttctg	tccttcaccc	gcctgctgct	gaattacagg	2400
aagtccctcc	gccatctggc	tgcttccatc	aacaagtttg	tgacgttcac	2450
ccataagtac	attacctaca	atgccccagc	agccatctcc	ttcctgcaga	2500
agcacgccga	cccgctccac	gacctgtcct	tcgacaacag	tgacctgggtg	2550
atgctgaaat	ccctccttgc	agggctcagc	ctgcccagca	gggacgacag	2600
gaccgaccga	ggcctggacg	aagagggcga	ggaggagagc	tcagccggct	2650

ccttgccctt ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700
 atggcccccct acatgaaacg gctttcccg ggcctaacgg tggaggatct 2750
 gctggagggtt ctgagtgaca tagacgagat gtcccggcgg agacccgaga 2800
 tcttgagctt cttctcgacc aacctgcagc ggctgatgag ctcgcccgag 2850
 gagtggttgc gcaacctcgc cttcagcctg gccctgcgct ccatgcagaa 2900
 cagccccagc attgcagccg ctttctgccc caggttcatt tactgcctgg 2950
 gcagccagga ctttgagggtg gtgcagacgg ccttcgggaa cctgcctgag 3000
 tacgctctcc tgtgccaaga gcacgcggct gtgctgctcc accgggcctt 3050
 cctggtgggc atgtacggcc agatggacc cagcgcgcag atctccgagg 3100
 ccttgaggat cctgcatatg gaggccgtga tgtgagcctg tggcagccga 3150
 cccccctcca agccccggcc cgtcccgctc cgggggatcc tcgaggcaaa 3200
 gccaggaag cgtgggcgtt gctggtctgt ccgaggaggt gagggcgcgc 3250
 agccctgagg ccaggcaggg ccaggagcaa tactccgagc cctgggggtgg 3300
 ctccggggcc gccgctggca tcagggggcc tccagcaagc cctcattcac 3350
 cttctggggc acagccctgc cgcggagcgg cggatcccc cgggcatggc 3400
 ctgggctggt tttgaatgaa acgacctgaa ctgtcaa 3437

<210> 22
 <211> 1029
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met His Ile Leu Val Val His Ala Met Val Ile Leu Leu Thr Leu
 1 5 10 15
 Gly Pro Pro Arg Ala Asp Asp Ser Glu Phe Gln Ala Leu Leu Asp
 20 25 30
 Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
 35 40 45
 Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
 50 55 60
 Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
 65 70 75
 Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
 80 85 90
 Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
 95 100 105

Gln	Ala	Val	Ala	His	Asp	Pro	Gln	Thr	Leu	Glu	Gln	Asn	Ile	Met	110	115	120
Asp	Lys	Asn	Tyr	Met	Ala	His	Leu	Val	Glu	Val	Gln	His	Glu	Arg	125	130	135
Gly	Ala	Ser	Gly	Gly	Gln	Thr	Phe	His	Ser	Leu	Leu	Thr	Ala	Ser	140	145	150
Leu	Pro	Pro	Arg	Arg	Asp	Ser	Thr	Glu	Ala	Pro	Lys	Pro	Lys	Ser	155	160	165
Ser	Pro	Glu	Gln	Pro	Ile	Gly	Gln	Gly	Arg	Ile	Arg	Val	Gly	Thr	170	175	180
Gln	Leu	Arg	Val	Leu	Gly	Pro	Glu	Asp	Asp	Leu	Ala	Gly	Met	Phe	185	190	195
Leu	Gln	Ile	Phe	Pro	Leu	Ser	Pro	Asp	Pro	Arg	Trp	Gln	Ser	Ser	200	205	210
Ser	Pro	Arg	Pro	Val	Ala	Leu	Ala	Leu	Gln	Gln	Ala	Leu	Gly	Gln	215	220	225
Glu	Leu	Ala	Arg	Val	Val	Gln	Gly	Ser	Pro	Glu	Val	Pro	Gly	Ile	230	235	240
Thr	Val	Arg	Val	Leu	Gln	Ala	Leu	Ala	Thr	Leu	Leu	Ser	Ser	Pro	245	250	255
His	Gly	Gly	Ala	Leu	Val	Met	Ser	Met	His	Arg	Ser	His	Phe	Leu	260	265	270
Ala	Cys	Pro	Leu	Leu	Arg	Gln	Leu	Cys	Gln	Tyr	Gln	Arg	Cys	Val	275	280	285
Pro	Gln	Asp	Thr	Gly	Phe	Ser	Ser	Leu	Phe	Leu	Lys	Val	Leu	Leu	290	295	300
Gln	Met	Leu	Gln	Trp	Leu	Asp	Ser	Pro	Gly	Val	Glu	Gly	Gly	Pro	305	310	315
Leu	Arg	Ala	Gln	Leu	Arg	Met	Leu	Ala	Ser	Gln	Ala	Ser	Ala	Gly	320	325	330
Arg	Arg	Leu	Ser	Asp	Val	Arg	Gly	Gly	Leu	Leu	Arg	Leu	Ala	Glu	335	340	345
Ala	Leu	Ala	Phe	Arg	Gln	Asp	Leu	Glu	Val	Val	Ser	Ser	Thr	Val	350	355	360
Arg	Ala	Val	Ile	Ala	Thr	Leu	Arg	Ser	Gly	Glu	Gln	Cys	Ser	Val	365	370	375
Glu	Pro	Asp	Leu	Ile	Ser	Lys	Val	Leu	Gln	Gly	Leu	Ile	Glu	Val	380	385	390
Arg	Ser	Pro	His	Leu	Glu	Glu	Leu	Leu	Thr	Ala	Phe	Phe	Ser	Ala			

	395		400		405
Thr Ala Asp Ala	Ala Ser Pro Phe Pro	Ala Cys Lys Pro Val	Val		
	410	415	420		
Val Val Ser Ser	Leu Leu Leu Gln Glu	Glu Glu Pro Leu Ala	Gly		
	425	430	435		
Gly Lys Pro Gly	Ala Asp Gly Gly Ser	Leu Glu Ala Val Arg	Leu		
	440	445	450		
Gly Pro Ser Ser	Gly Leu Leu Val Asp	Trp Leu Glu Met Leu	Asp		
	455	460	465		
Pro Glu Val Val	Ser Ser Cys Pro Asp	Leu Gln Leu Arg Leu	Leu		
	470	475	480		
Phe Ser Arg Arg	Lys Gly Lys Gly Gln	Ala Gln Val Pro Ser	Phe		
	485	490	495		
Arg Pro Tyr Leu	Leu Thr Leu Phe Thr	His Gln Ser Ser Trp	Pro		
	500	505	510		
Thr Leu His Gln	Cys Ile Arg Val Leu	Leu Gly Lys Ser Arg	Glu		
	515	520	525		
Gln Arg Phe Asp	Pro Ser Ala Ser Leu	Asp Phe Leu Trp Ala	Cys		
	530	535	540		
Ile His Val Pro	Arg Ile Trp Gln Gly	Arg Asp Gln Arg Thr	Pro		
	545	550	555		
Gln Lys Arg Arg	Glu Glu Leu Val Leu	Arg Val Gln Gly Pro	Glu		
	560	565	570		
Leu Ile Ser Leu	Val Glu Leu Ile Leu	Ala Glu Ala Glu Thr	Arg		
	575	580	585		
Ser Gln Asp Gly	Asp Thr Ala Ala Cys	Ser Leu Ile Gln Ala	Arg		
	590	595	600		
Leu Pro Leu Leu	Leu Ser Cys Cys Cys	Gly Asp Asp Glu Ser	Val		
	605	610	615		
Arg Lys Val Thr	Glu His Leu Ser Gly	Cys Ile Gln Gln Trp	Gly		
	620	625	630		
Asp Ser Val Leu	Gly Arg Arg Cys Arg	Asp Leu Leu Leu Gln	Leu		
	635	640	645		
Tyr Leu Gln Arg	Pro Glu Leu Arg Val	Pro Val Pro Glu Val	Leu		
	650	655	660		
Leu His Ser Glu	Gly Ala Ala Ser Ser	Ser Val Cys Lys Leu	Asp		
	665	670	675		
Gly Leu Ile His	Arg Phe Ile Thr Leu	Leu Ala Asp Thr Ser	Asp		
	680	685	690		

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys	695	700	705
Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Arg His Leu	710	715	720
Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe	725	730	735
Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val	740	745	750
Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu	755	760	765
His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu	770	775	780
Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile	785	790	795
Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala	800	805	810
Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His	815	820	825
Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu	830	835	840
Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg	845	850	855
Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu	860	865	870
Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu	875	880	885
Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu	890	895	900
Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg	905	910	915
Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu	920	925	930
Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu	935	940	945
Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe	950	955	960
Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val	965	970	975
Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys			

980	985	990
Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly		
995	1000	1005
Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu		
1010	1015	1020
Arg Ile Leu His Met Glu Ala Val Met		
1025		

<210> 23
 <211> 2186
 <212> DNA
 <213> Homo sapiens

<400> 23
 ccgggccatg cagcctcggc cccgcgggag cccgcgcgcg acccgaggag 50
 atgaggctcc gcaatggcac ctctctgacg ctgctgctct tetgctgtg 100
 cgccttctct tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150
 acgttggtga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200
 cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250
 gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300
 gagacggcaa tcgcacctgg ggcgcctaa cagaggaccc ccgattgaag 350
 ccgtggaacg gctcacaccg gcacgtgctg cacctgccc cgtcttcca 400
 tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450
 gcgtgggcca gggccgcacc ggagtgtcgg tggatgatgg catcccgagc 500
 gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550
 ctccgagctg agcccgagg agaaggagga ctcggtcatc gtggtgctga 600
 tcgccgagac tgactcacag tacacttcgg cagtgcaga gaacatcaag 650
 gccttggtcc ccacggagat ccattctggg ctctggagg tcattctacc 700
 cteccccac ttctacctg acttctcccg cctccgagag tcctttgggg 750
 accccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800
 ttctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850
 ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900
 cactgcagca gccttcagag gactggatga tcctggagtt ctccagctg 950
 ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000
 gttcattctc atgttctacc gggacaagcc catcgactgg ctctggacc 1050

atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100
 gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150
 gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200
 acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgccca 1250
 gcagaggtga gcacgagcct gaagacatac cagcacttca ccctggagaa 1300
 agcctacctg cgcgaggact tcttctgggc cttcaccctt gccgcggggg 1350
 acttcatcgc cttccgcttc ttccaacctc taagactgga gcggttcttc 1400
 ttccgcagtg ggaacatcga gcacccggag gacaagctct tcaacacgtc 1450
 tgtggaggtg ctgcccttcg acaacctca gtcagacaag gaggccctgc 1500
 aggagggccg caccgccacc ctccggtacc ctccgagccc cgacggctac 1550
 ctccagatcg gctccttcta caagggagtg gcagaggag aggtggaccc 1600
 agccttcggc cctctggaag cactgcgcct ctcgatccag acggactccc 1650
 ctgtgtgggt gattctgagc gagatcttcc tgaaaaaggc cgactaagct 1700
 gggggtctct gaggggtacc tgtggccagc cctgaagccc acatttctgg 1750
 ggggtgtcgc actgccgtcc ccggagggcc agatacggcc ccgccccaaag 1800
 ggttctgcct ggcgtcgggc ttgggcccgc ctgggggtccg ccgctggccc 1850
 ggagggcccta ggagctggtg ctgccccgc ccgcccgggc gcggaggagg 1900
 caggcggccc ccacactgtg cctgaggccc ggaaccgttc gcacccggcc 1950
 tgccccagtc aggcggtttt agaagagctt ttacttgggc gccgcgcgtc 2000
 tctggcgcca acactggaat gcataacta ctttatgtgc tgtgtttttt 2050
 attcttggtt acatttgatt ttttcacgta agtccacata tacttctata 2100
 agagcgtgac ttgtaataaa gggttaatga agaaaaaaaa aaaaaaaaaa 2150
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186

<210> 24
 <211> 548
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Arg Leu Arg Asn Gly Thr Phe Leu Thr Leu Leu Phe Cys
 1 5 10 15
 Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly
 20 25 30

Gln	Lys	Gly	Asp	Val	Val	Asp	Val	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	
				35					40					45	
Leu	Arg	Asp	Arg	Leu	His	Ala	Ala	Glu	Gln	Glu	Ser	Leu	Lys	Arg	
				50					55					60	
Ser	Lys	Glu	Leu	Asn	Leu	Val	Leu	Asp	Glu	Ile	Lys	Arg	Ala	Val	
				65					70					75	
Ser	Glu	Arg	Gln	Ala	Leu	Arg	Asp	Gly	Asp	Gly	Asn	Arg	Thr	Trp	
				80					85					90	
Gly	Arg	Leu	Thr	Glu	Asp	Pro	Arg	Leu	Lys	Pro	Trp	Asn	Gly	Ser	
				95					100					105	
His	Arg	His	Val	Leu	His	Leu	Pro	Thr	Val	Phe	His	His	Leu	Pro	
				110					115					120	
His	Leu	Leu	Ala	Lys	Glu	Ser	Ser	Leu	Gln	Pro	Ala	Val	Arg	Val	
				125					130					135	
Gly	Gln	Gly	Arg	Thr	Gly	Val	Ser	Val	Val	Met	Gly	Ile	Pro	Ser	
				140					145					150	
Val	Arg	Arg	Glu	Val	His	Ser	Tyr	Leu	Thr	Asp	Thr	Leu	His	Ser	
				155					160					165	
Leu	Ile	Ser	Glu	Leu	Ser	Pro	Gln	Glu	Lys	Glu	Asp	Ser	Val	Ile	
				170					175					180	
Val	Val	Leu	Ile	Ala	Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Ala	Val	
				185					190					195	
Thr	Glu	Asn	Ile	Lys	Ala	Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	Gly	
				200					205					210	
Leu	Leu	Glu	Val	Ile	Ser	Pro	Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe	
				215					220					225	
Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly	Asp	Pro	Lys	Glu	Arg	Val	Arg	
				230					235					240	
Trp	Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	
				245					250					255	
Ala	Gln	Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln	Leu	Glu	Asp	Asp	Ile	
				260					265					270	
Val	Ala	Lys	Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys	Asn	Phe	Ala	Leu	
				275					280					285	
Gln	Gln	Pro	Ser	Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu	
				290					295					300	
Gly	Phe	Ile	Gly	Lys	Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser	Leu	Ile	
				305					310					315	
Val	Glu	Phe	Ile	Leu	Met	Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp	Trp	

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

320	325	330
Leu Leu Asp His Ile Leu Trp Val Lys	Val Cys Asn Pro Glu Lys	
335	340	345
Asp Ala Lys His Cys Asp Arg Gln Lys	Ala Asn Leu Arg Ile Arg	
350	355	360
Phe Lys Pro Ser Leu Phe Gln His Val	Gly Thr His Ser Ser Leu	
365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp	Lys Asp Phe Gly Lys Gln	
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro	Pro Ala Glu Val Ser Thr	
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr	Leu Glu Lys Ala Tyr Leu	
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr	Pro Ala Ala Gly Asp Phe	
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu	Arg Leu Glu Arg Phe Phe	
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro	Glu Asp Lys Leu Phe Asn	
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp	Asn Pro Gln Ser Asp Lys	
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala	Thr Leu Arg Tyr Pro Arg	
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly	Ser Phe Tyr Lys Gly Val	
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe	Gly Pro Leu Glu Ala Leu	
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro	Val Trp Val Ile Leu Ser	
530	535	540
Glu Ile Phe Leu Lys Lys Ala Asp		
545		

<210> 25

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 25

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 26
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 27
actcgggatt cctgctgtt 19

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 28
aggcctttac ccaaggccac aac 23

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 29
ggcctgtcct gtgttctca 19

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 30
tcccaccact tacttccatg aa 22

<210> 31
<211> 25
<212> DNA

[illegible]

<220>

<223> Synthetic Oligonucleotide Probe

<400> 36

ccagtcaggc cgtttttaga 19

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 37

cgggcgccca agtaaaagct c 21

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 38

cataaagtag tatatgcatt ccagtgtt 28

ccagtcaggc cgtttttaga 19
cgggcgccca agtaaaagct c 21
cataaagtag tatatgcatt ccagtgtt 28